

# Aminoacid sequence

Alignment Report of Untitled ClustalV (PAM250)

viernes, 19 de diciembre de 2008 19:38

1	MAERVLTIRVHSLRERVDATLA AHRNEILLFLSRIESHSGKG	WT
1	MAERVLTIRVHSLRERVDATLA AHRNEILLFLSRIESHSGKG	S85
41	ILKPHELLLAEEFDAIRQDDKNKLN EHA FEEL LKSTQEAI VL	WT
41	ILKPHELLLAEEFDAIRQDDKNKLN EHA FEEL LKSTQEAI VL	S85
81	PFWVALAIRLRPGVWEYIRVNVNAL LVVEELSVSEY LQFKE	WT
81	PFWVALAIRLRPGVWEYIRVNVNAL LVVEELSVSEY LQFKE	S85
101	ELVDGASNGNFEVLELDFEFPFTAS FPKPTLTNKSIGNGV EFL	WT
101	ELVDGASNGNFEVLELDFEFPFTAS FPKPTLTNKSIGNGV EFL	S85
161	NRHLSAKMFHDKESMTPLLEFLRAH HYKGMTMMLNDRIQN	WT
161	NRHLSAKMFHDKESMTPLLEFLRAH HYKGMTMMLNDRIQN	S85
201	SNTLQNVLRKAEEYLLIMLSFDTPY FEFERHNFQEIGLEK GW	WT
201	SNTLQNVLRKAEEYLLIMLSFDTPY FEFERHNFQEIGLEK GW	S85
241	GDTAERVLEKMCMLDLDLLEAPDGS OTLEKFLGRIPMVFN VV	WT
241	GDTAERVLEKMCMLDLDLLEAPDGS OTLEKFLGRIPMVFN VV	S85
281	ILSPHGYFAQENVLGYPD TGGQVVYILDQVPALER EMLKR	WT
281	ILSPHGYFAQENVLGYPD TGGQVVYILDQVPALER EMLKR	S85
321	IKEQGGLDIIPRILIVTRLLLPDA VGTTGQQRIEK VYGA EHS	WT
321	IKEQGGLDIIPRILIVTRLLLPDA VGTTGQQRIEK VYGA EHS	S85
361	HILRVPFERTEKGI VRK WIS RFEVWSPYMETFIEDV AKEISA	WT
361	HILRVPFERTEKGI VRK WIS RFEVWSPYMETFIEDV AKEISA	S85
401	ELQAKPDLLIIGNYSEGNLAASLLA HKLGVTQCTIAHALEK	WT
401	ELQAKPDLLIIGNYSEGNLAASLLA HKLGVTQCTIAHALEK	S85
441	TKYPDSDIYWKKFDEK YH FESSQFTADLIAMNHTDFIITST	WT
441	TKYPDSDIYWKKFDEK YH FESSQFTADLIAMNHTDFIITST	S85
481	FQEIAGSKDITVGQYESHMAFTMPGL YRVVHGINVFDPKFEN	WT
481	FQEIAGSKDITVGQYESHMAFTMPGL YRVVHGINVFDPKFEN	S85
521	IVSPGADINLYFSYSETEKRLTA FHPEIDELLYSDV ENDE	WT
521	IVSPGADINLYFSYSETEKRLTA FHPEIDELLYSDV ENDE	S85
561	HLCVLKDRTKPILFTMARLDRVKNLT GLVSWYAKNPRLRG	WT
561	HLCVLKDRTKPILFTMARLDRVKNLT GLVSWYAKNPRLRG	S85
601	LVNLVVVVGDDRKESKDLEEQAEMKK MYELIETHNLNGQF	WT
601	LVNLVVVVGDDRKESKDLEEQAEMKK MYELIETHNLNGQF	S85
641	RWISSQMNRVVRNGELYRYIADTKGA FVQPAFYEA FGLTIVV	WT
641	RWISSQMNRVVRNGELYRYIADTKGA FVQPAFYEA FGLTIVV	S85
681	EAMTCGLPTTFATNHGGPAEII VHGKSGFHI DPYHGEQAAD	WT
681	EAMTCGLPTTFATNHGGPAEII VHGKSGFHI DPYHGEQAAD	S85
721	LLADFFFEKCKKEP SHWETISTGGLKRIQEKYTWQIY SERL	WT
721	LLADFFFEKCKKEP SHWETISTGGLKRIQEKYTWQIY SERL	S85
761	LTLAADVYGFWKHVSKLDRLEIRRYLE MFYALKYRKMAEAV	WT
761	LTLAADVYGFWKHVSKLDRLEIRRYLE MFYALKYRKMAEAV	S85
801	PLAAE	WT
801	PLAAE	S85

## Nucleotide sequence

### Alignment Report of Untitled ClustalV (Weighted)

viernes, 19 de diciembre de 2008 19:36

1	ATGGGCTGAACGCTGTTTGTGACTCGTGTGTTTCATAGCCCTTCGGTG	WT
1	ATGGGCTGAACGCTGTTTGTGACTCGTGTGTTTCATAGCCCTTCGGTG	SS5
41	AACGTGTGTGATGCAACCTTTAGCTGCTCACCAGCAATGAGAT	WT
41	AACGTGTGTGATGCAACCTTTAGCTGCTCACCAGCAATGAGAT	SS5
81	ACIGCTGTGTTTCTTTTCAAGGATCGAAAGCCACGGGAAAAGGG	WT
81	ACIGCTGTGTTTCTTTTCAAGGATCGAAAGCCACGGGAAAAGGG	SS5
121	ATATTGAAACCTTCATGAGCTTTTGGCTGAGTTTCGATGCAA	WT
121	ATATTGAAACCTTCAGGAGCTTTTGGCTGAGTTTCGATGCAA	SS5
161	TTCGCCAAGATGACAAAAACAACCTGAACGAAACATGCATT	WT
161	TTCGCCAAGATGACAAAAACAACCTGAACGAAACATGCATT	SS5
201	CGAAGAACTTCCTGAAATCCACTCAGGAAGCGATTGTTCTG	WT
201	CGAAGAACTTCCTGAAATCCACTCAGGAAGCGATTGTTCTG	SS5
241	CCCCCTTGGGGTTGCACTTGCTATTGCTTTGAGGCCCTGGTG	WT
241	CCCCCTTGGGGTTGCACTTGCTATTGCTTTGAGGCCCTGGTG	SS5
281	TCIGGGGAATACATCCGTTGTGAACGTCGAATGCACTAGTTGT	WT
281	TCIGGGGAATACATCCGTTGTGAACGTCGAATGCACTAGTTGT	SS5
321	CGAGGAGCTGTCTCCGTCCCTGAGTAATTGCAATTCGAAGGAA	WT
321	CGAGGAGCTGTCTCCGTCCCTGAGTAATTGCAATTCGAAGGAA	SS5
361	GAACTTGTTCGACGGAGCCCTCGAATGGAAATTTTGTCTCTCG	WT
361	GAACTTGTTCGACGGAGCCCTCGAATGGAAATTTTGTCTCTCG	SS5
401	AGTTGGATTTCGAGCCCTTTCACCTGCATCCCTTTCCTAAACCC	WT
401	AGTTGGATTTCGAGCCCTTTCACCTGCATCCCTTTCCTAAACCC	SS5
441	AACCCCTCACCAAAATCTATTGGAAATGGAGTTGAATTTCCTC	WT
441	AACCCCTCACCAAAATCTATTGGAAATGGAGTTGAATTTCCTC	SS5
481	AATAGGCACCTCTCTGCCCCAAAATGTTCCATGACAAAGGAAA	WT
481	AATAGGCACCTCTCTGCCCCAAAATGTTCCATGACAAAGGAAA	SS5
521	GCATGACCCCGCTTCTCGAATTTCTTCGCGGCTCACCCATT	WT
521	GCATGACCCCGCTTCTCGAATTTCTTCGCGGCTCACCCATT	SS5
561	TAAGGGCAAGACCAATGATGCTGAATGATAGGATACAGAAT	WT
561	TAAGGGCAAGACCAATGATGCTGAATGATAGGATACAGAAT	SS5
601	TCGAATACTCTTCAAAATGTTCCCTAAGGAAGGCAGAGGAAT	WT
601	TCGAATACTCTTCAAAATGTTCCCTAAGGAAGGCAGAGGAAT	SS5
641	ACCTCATTTATGCTTTTCCCCAGATACTCCCATATTTTCGAATT	WT
641	ACCTCATTTATGCTTTTCCCCAGATACTCCCATATTTTCGAATT	SS5
681	CGAGCACCAAGITCCCAAGAAATCGGATTGGAGAAAGGGATGG	WT
681	CGAGCACCAAGITCCCAAGAAATCGGATTGGAGAAAGGGATGG	SS5
721	GGGGACACGGCGGGAGCGTGTGCTAGAGATGGTATGCATGC	WT
721	GGGGACACGGCGGGAGCGTGTGCTAGAGATGGTATGCATGC	SS5
761	TTCTTGATCTCTCTTGAGGCTCCTGACTCATGTACTCTCTGA	WT
761	TTCTTGATCTCTCTTGAGGCTCCTGACTCATGTACTCTCTGA	SS5
801	GAAGTTCCTTGGGGGAGAATTCCCTATGGTTTTCGAATGTGGTT	WT
801	GAAGTTCCTTGGGGGAGAATTCCCTATGGTTTTCGAATGTGGTT	SS5

241 ATCCCTTTTCCCCCTCATGGGATATTTTGGCCCAAGAAAAATGTCT WT  
 241 ATCCCTTTTCCCCCTCATGGGATATTTTGGCCCAAGAAAAATGTCT SS5  
  
 281 TGGGTTTATCCCCGACACCGGTGGGCCAGGTTGTCTACATTTT WT  
 281 TGGGTTTATCCCCGACACCGGTGGGCCAGGTTGTCTACATTTT SS5  
  
 321 AGATCAAGTTTCCCCGCCCTTGGAGCGGTGAAATGCTTAAGCGC WT  
 321 AGATCAAGTTTCCCCGCCCTTGGAGCGGTGAAATGCTTAAGCGC SS5  
  
 361 ATAAAGGAGCAAGGACTTGATATCATCCCCCGIATTTCTTA WT  
 361 ATAAAGGAGCAAGGACTTGATATCATCCCCCGIATTTCTTA SS5  
  
 1001 TTGTTACTCTGCTCTGCTGCCCCGATGCGAGTTGGAAACCACTTG WT  
 1001 TTGTTACTCTGCTCTGCTGCCCCGATGCGAGTTGGAAACCACTTG SS5  
  
 1041 TGGTTCAGAGGATTGAGAAAGGTGTATGGAGCAGAAACACTCA WT  
 1041 TGGTTCAGAGGATTGAGAAAGGTGTATGGAGCAGAAACACTCA SS5  
  
 1081 CATATTCTTAGGGTCCCTTTTAGGACTGAGAAAGGGCATTTG WT  
 1081 CATATTCTTAGGGTCCCTTTTAGGACTGAGAAAGGGCATTTG SS5  
  
 1121 TTCGCCAAATGGGATCTCTCGCTTTTGAAGTGTGGCCATACAT WT  
 1121 TTCGCCAAATGGGATCTCTCGCTTTTGAAGTGTGGCCATACAT SS5  
  
 1161 GGAGACATTTCATTGAGGATGTGTGCCAAAAGAAATTTCTTCCA WT  
 1161 GGAGACATTTCATTGAGGATGTGTGCCAAAAGAAATTTCTTCCA SS5  
  
 1201 GAACTGCGAGGCCAAGCCAGATTITGATAAATTGGAAACTACA WT  
 1201 GAACTGCGAGGCCAAGCCAGATTITGATAAATTGGAAACTACA SS5  
  
 1241 GTGAGGGGCAATCTTTGCTGCTTCTTTTGGCTAGCTCCACAAGTT WT  
 1241 GTGAGGGGCAATCTTTGCTGCTTCTTTTGGCTAGCTCCACAAGTT SS5  
  
 1281 AGGCGTAACTCAGTGCACCATTTGCCCACGCGTTGGAGAAAA WT  
 1281 AGGCGTAACTCAGTGCACCATTTGCCCACGCGTTGGAGAAAA SS5  
  
 1321 ACGAAGTATCCTTGATTCCGACATTCTTACTGGAAAAAGTTTG WT  
 1321 ACGAAGTATCCTTGATTCCGACATTCTTACTGGAAAAAGTTTG SS5  
  
 1361 ATGAAAAAATACCATTTCTCTGCTCCAGTTTACCGCTGATCT WT  
 1361 ATGAAAAAATACCATTTCTCTGCTCCAGTTTACCGCTGATCT SS5  
  
 1401 CATTGCCAATGAATCACACTGATTTCATCATCACCAAGCACCC WT  
 1401 CATTGCCAATGAATCACACTGATTTCATCATCACCAAGCACCC SS5  
  
 1441 TTCCAGGAGATAGCAGGAAGCAAGGACACCTGTAGGACAAT WT  
 1441 TTCCAGGAGATAGCAGGAAGCAAGGACACCTGTAGGACAAT SS5  
  
 1481 ATGAGAGCCCATATGGGCATTACACAAIGCCCTGGATTGTACAG WT  
 1481 ATGAGAGCCCATATGGGCATTACACAAIGCCCTGGATTGTACAG SS5  
  
 1521 AGTTGTTCACCGGCATTAAATGTGTTTCGACCCCAAAATTC AAC WT  
 1521 AGTTGTTCACCGGCATTAAATGTGTTTCGACCCCAAAATTC AAC SS5  
  
 1561 ATTGTCTCACCTGGAGCTGATATTAAATCTCTACTTCTCGT WT  
 1561 ATTGTCTCACCTGGAGCTGATATTAAATCTCTACTTCTCGT SS5  
  
 1601 ACTCCGAAACGGAGAAGAGACTTACAGCATTTTCAACCCTGA WT  
 1601 ACTCCGAAACGGAGAAGAGACTTACAGCATTTTCAACCCTGA SS5  
  
 1641 AATTGATGAGCTGCTGTATAGTGAAGTTGAGAAATGACGAG WT  
 1641 AATTGATGAGCTGCTGTATAGTGAAGTTGAGAAATGACGAG SS5

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1681 C A T C T G T G T G T G C T C A A G G A C A G G A C T A A A C C A A T T T T A T WT
1681 C A T C T G T G T G T G C T C A A G G A A A G G A C T A A A C C A A T T T T A T SS5

1721 T C A C A A A T G G C A A G G T T G G A T C G T G T G A A G A A T T T A A C T G G WT
1721 T C A C A A A T G G C A A G G T T G G A T C G T G T G A A G A A T T T A A C T G G SS5

1761 A C I T G T T G A G T G G T A C G C C A A G A A T C C A C G A C T A A G G G G A WT
1761 A C I T G T T G A G T G G T A C G C C A A G A A T C C A C G A C T A A G G G G A SS5

1801 T T G G T T A A C C T G G I T G T A G T T G G C G G A G A T C G A A G G A A G G WT
1801 T T G G T T A A C C T G G I T G T A G T T G G C G G A G A T C G A A G G A A G G SS5

1841 A A T C C A A A G A T T T G G A A G A G C A G G C A G A G A T G A A G A A G A T WT
1841 A A T C C A A A G A T T T G G A A G A G C A G G C A G A G A T G A A G A A G A T SS5

1881 G T A T G A G C T A A E T T G A G A C T C A T A A A T T T G A A T G G C C A A T T C WT
1881 G T A T G A G C T A A T A G A G A C T C A T A A A T T T G A A T G G C C A A T T C SS5

1921 A G A T G G A T T T T C T T C C C A G A T G A A C C G A G T G A G G A A T G G T G WT
1921 A G A T G G A T T T T C T T C C C A G A T G A A C C G A G T G A G G A A T G G T G SS5

1961 A G C T C T A C C G A T A C A T T G C T G A C A C T A A G G G A G C T T T C G T WT
1961 A G C T C T A C C G A T A C A T T G C T G A C A C T A A G G G A G C T T T C G T SS5

2001 T C A G C C T G C A T T C I A C G A G G C C T T T G G T C I G A C T G T T G T C WT
2001 T C A G C C T G C A T T C I A C G A G G C A T T T G G T C T G A C T G T T G T C SS5

2041 G A A G C A A T G A C T T G T G G T T T G C C T A C A T T T G C A A C T A A T C WT
2041 G A A G C A A T G A C T T G T G G T T T G C C T A C A T T T G C A A C T A A T C SS5

2081 A C G G T G G T C C A G C T G A G A T C A T C G I T C A T G G A A A G T C C G G WT
2081 A C G G T G G T C C A G C T G A G A T C A T C G I T C A T G G A A A G T C C G G SS5

2121 C T T C C A C A T T G A T C C A T A T C A C G G I G A G C A A G C T G C T G A T WT
2121 C T T C C A C A T T G A T C C A T A T C A C G G I G A G C A A G C T G C T G A T SS5

2161 C T G C T A G C T G A T T T C T T T G A G A A A T G C A A G A A A G A G C C T T WT
2161 C T G C T A G C T G A T T T C T T T G A G A A A T G C A A G A G A G A G C C T T SS5

2201 C A C A T T G G G A A A C C A T T T C G A C G G G T G G C C T G A A G C G C A T WT
2201 C A C A T T G G G A A A C C A T T T C G A C G G A T G G C C T G A A G C G C A T SS5

2241 C C A A G A G A A G T A C A C T T G G C A A A T C T A C T C C G A A A G G C T A WT
2241 C C A A G A G A A G T A C A C T T G G C A A A T C T A C T C C G A A A G G C T A SS5

2281 T T G A C A C T G G C T G C T G T T T A T G G G I T C T G G A A A C A T G T T T WT
2281 T T G A C A C T G G C T G C T G T T T A T G G G I T C T G G A A A C A T G T T T SS5

2321 C T A A A C T T G A T C G T C T A G A A A T C C G T C G C T A T C T T G A A A T WT
2321 C T A A G C T T G A T C G T C T A G A A A T C C G T C G C T A T C T T G A A A T SS5

2361 G T I T T A T G C T C T C A A G T A C C G T A A G A T G G C T G A A G C T G T T WT
2361 G T I T T A T G C T C T C A A G T A C C G T A A G A T G G C T G A A G C T G T T SS5

2401 C C A T T G G C T G C T G A G T G A WT
2401 C C A T T G G C T G C T G A G T G A SS5

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Decoration 'Decoration #1': Shade (with solid deep red) residues that differ from SSX.